

ID	Q9VDN2	PRELIMINARY;	PRT;	43 AA.
DT	01-MAY-2000 (TrEMBLrel. 13, Created)			
DT	01-MAY-2000 (TrEMBLrel. 13, Last sequence update)			
DT	01-JUN-2000 (TrEMBLrel. 14, Last annotation update)			
DE	CG5097 PROTEIN.			
GN	CG5097.			
OS	Drosophila melanogaster (Fruit fly).			
OC	Eukaryota; Metazoa; Anthropoda; Tracheata; Hexapoda; Insecta;			
OC	Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;			
OC	Ephydroidea; Drosophilidae; Drosophila.			
OX	NCBI_TaxId=7227;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=BERKELEY;			
RX	MEDLINE=20196006; PubMed=10731132;			
RA	Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,			
RA	Mananides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,			
RA	George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,			
RA	Sulton G.G., Wortman J.R., Yancelli M.D., Zhang Q., Chen L.X.,			
RA	Brandon R.C., Rogers Y.-H.C., Blazer R.G., Champe M., Pfeiffer B.D.,			
RA	Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,			
RA	April J.F., Aghayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,			
RA	Bailey R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,			
RA	Beeson K.Y., Benos P.V., Beremand B.P., Bhattacharya D., Bolshakov S.,			
RA	Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotlier P.,			
RA	Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,			
RA	Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,			
RA	de Paulos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,			
RA	Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,			
RA	Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,			
RA	Foster C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,			
RA	Glodde A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,			
RA	Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,			
RA	Hoslin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,			
RA	Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Kelthum K.A.,			
RA	Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,			
RA	Lasko P., Lai Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,			
RA	Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,			
RA	Merkulov G., Milshina N.V., Moberly C., Morris J., Moshrefi A.,			
RA	Mount S.M., Moy M., Murphy B., Murphy L., Munz D.M., Nelson D.L.,			
RA	Nelson D.R., Nelson K.A., Nixon K., Nusslein D.R., Pacle J.M.,			
RA	Palazzolo M., Piltman G.S., Pan S., Pollard J., Puri V., Reese M.G.,			
RA	Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,			
RA	Shue B.C., Siden-Kiamos I., Simpson K., Skupski M.P., Smith T.,			
RA	Spieler E., Spradling A.C., Stapleton M., Strong R., Sun E.,			
RA	Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,			
RA	Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weisenbach J.,			
RA	Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,			
RA	Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,			
RA	Zhang X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X.,			
RA	Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;			
RT	"The genome sequence of <i>Drosophila melanogaster</i> ."			
RL	Science 287:2185-2195(2000).			
RU	EMBL: AE003730; AAF55758.1;			
DR	FLYBASE: FBgn0038790; CG5097.			
DR	INTERPRO: IPR000561;			
DR	INTERPRO: IPR000966;			
DR	PFAM: PF02067; Metallothio_5; 1.			
DR	PRINTS: PR00872; MTDIPTEA.			
DR	PROSITE: PS00022; EGF_1; UNKNOWN_1.			
QO	SEQUENCE 43 AA: 4597 MW: E54E722B14EB9DDE CRC64:			

Query Match	100.0%	Score 54	DB 5	Length 43
Best Local Similarity	18.2%	Pred.No. 75		
Matches	4	Conservative	18	Mismatches 0; Indels 0; Gaps 0

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QY 1 CXXXXXXXXXXXXXXXXCXXXC 22
    |::|:::|:::|:::|:::|:::|
Db 6 CGTNCCKQDPTKCGDNCACNQDC 27
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SEQUENCE	44 AA:	4892 MW:	59F2E69015593F8C CR664:
SO	NON_TER	1	1
FT	NON_TER	44	44
DR	PROSITE: PS00427; DISINTEGRIN_1; 1.		
DR	PFAM: PF00200; disintegrin; 1.		
DR	SMART: SM001762; -		
DR	MED: MGI:105987; Adam32.		
DR	HSSP: P17347; 2ECH.		
DR	EMBL: U06147; AAA18426.1; -.		
RL	Proc. Natl. Acad. Sci. U.S.A. 91:2748-2751(1994).		
RT	"A family of cellular proteins related to snake venom disintegrins."		
RA	Weekamp G., Blobel C.P.;		
RC	STRAIN-BALB/C;		
RX	MEDLINE=94195820; PubMed=8146185;		
RP	NCBI_TaxID=10090;		
RR	[1]		
RS	SEQUENCE FROM N.A.		
SC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OS	Mus musculus (Mouse).		
GN	Adam32 OR DTGN2.		
DE	DISINTEGRIN 2 (CELLULAR DISINTEGRIN-RELATED PROTEIN) (FRAGMENT).		
DT	01-JUL-2000 (Tremblrel. 15, last annotation update)		
DT	01-JUL-1997 (Tremblrel. 04, last sequence update)		
AC	Q06020;		
ID	Q06020	PRELIMINARY;	PRT; 44 AA.
RESULT	3		

Query Match	100.0%;	Score 54;	DB 11;	Length 44;
Best Local Similarity	18.2%;	Pred. No. 76;		
Matches 4;	Conservative 18;	Mismatches 0;	Indels 0;	Gaps 0

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QY 1 CXXXXXXXXXXXXXXXXC 22
    |::|:::|:::|:::|
Db 9 CEPTCLKKDAECSHGLCN 30
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Q	FT	DR	FT	Q
SEQUENCE	46 AA;	5061 MW;	311922EPB40A44E8F	CRC64;
NON_TER	1	1		
EMBL:	U63332;	AAB05810.1;	-	
RA	Submitted (JUL-1996)	to the EMBL/Genbank/DBJ	databases.	
RL				
RA	Lemasson I., Devaux C., Mesnard J.M.;			
RN	SEQUENCE FROM N.A.			
RP				
OX	NCBI_TaxID=9606;			
OC	Mammalia: Eutheria; Primates; Catarrhini; Hominiidae; Homo.			
CC				
DE	Homo sapiens (Human).			
DE	CSTEINE-RICH PROTEIN (FRAGMENT).			
DT	01-NOV-1996 (TREMBLrel. 01, Last sequence update)			
DT	01-AUG-1998 (TREMBLrel. 07, Last annotation update)			
AC	016861;			
ID	016861	PRELIMINARY;	PRT;	46 AA.
RESULT	4			

Query Match	100.0%	Score 54	DB 4	Length 46
Best Local Similarity	18.2%	Pred. No. 78		
Matches 4	Conservative 18	Mismatches 0	Indels 0	Gaps 0

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Qy 1 CXXXXXXXXXXXXXXXXC 22
    |::|:::|:::|:::|
Db 11 CCCCCCCCCCCCCCCCCC 32
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RESULT 5
Q060622
ID Q060622 PRELIMINARY; PRT; 46 AA

RESULT	9		
042597			
ID	042597	PRELIMINARY;	PRT: 49 AA
AC	042597;		
DT	01-JAN-1998	(TREMBLrel. 05, Created)	

DT 01-JAN-1998 (TREMBLrel. 05, last sequence update)
 DE METALLOPROTEASE/DISINTEGRIN XMDCL1.1 (FRAGMENT).
 OC Xenopus laevis (African clawed frog).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidea; Pipidae;
 OC Xenoportidae; Xenopus.
 NCBI_TaxID=8355;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=TESTIS;
 RX MEDLINE=97349132; PubMed=9205136;
 RA Shilling F.M., Kratzschmar J., Cai H., Weskamp G., Gayko U.,
 RA Leibow J., Myles D.G., Nuccitelli R., Blobel C.P.;
 RT "Identification of metalloprotease/disintegrins in Xenopus laevis
 RT testis with a potential role in fertilization".
 RL Dev. Biol. 186:155-164(1997).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=TESTIS;
 RA Kratzschmar J., Cai H., Blobel C.P.;
 RL Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.
 DR EMBL; U78189; AAB87149.1; -;
 DR HSSP; P17494; 1KST.
 DR INTERPRO: IPR001762; -;
 DR PFAM; PF00200; disintegrin.1.
 KW Integrin; Protease; Metalloprotease.
 FT NON_TER 1
 FT SEQUENCE 49 AA; 5316 MW; EFBDAE74DA582609 CRC64;

Query Match 100.0%; Score 54; DB 13; Length 49;
 Best Local Similarity 18.2%; Pred. No. 81;
 Matches 4; Conservative 18; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CXXXCXXXXXXXXXXCXXC 22
 Db 13 CCKCTLSHDMCSDGLCRGC 34

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RESULT 10
 ID 008636 PRELIMINARY; PRT; 54 AA.
 AC 008636;
 DT 01-JUL-1997 (TREMBLrel. 04, Created)
 DT 01-JUL-1997 (TREMBLrel. 04, last sequence update)
 DT 01-NOV-1999 (TREMBLrel. 12, last annotation update)
 DE HIGH-GLYCINE TYROSINE KERATIN TYPE II.3 (FRAGMENT).
 GN KRAP6-3.
 OS Mus musculus (Mouse).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
 NCBI_TaxID=10090;
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=SKIN;
 RA Aoki N.;
 RL Submitted (DEC-1996) to the EMBL/GenBank/DBJ databases.
 DR EMBL; D89901; BAA19687.1; -;
 DR MGD; MGI:1330279; Krtap6-3.
 KW Keratin.
 FT NON_TER 1
 FT SEQUENCE 54 AA; 5729 MW; 2E7880E8822C1787 CRC64;

Query Match 100.0%; Score 54; DB 11; Length 54;
 Best Local Similarity 18.2%; Pred. No. 86;
 Matches 4; Conservative 18; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CXXXCXXXXXXXXXXCXXC 22
 Db 25 CGGCGYGGYGGYGGCCSPLC 46

RESULT 11
 ID 09N9H2 PRELIMINARY; PRT; 57 AA.
 AC 09N9H2;
 DT 01-OCT-2000 (TREMBLrel. 15, Created)
 DT 01-OCT-2000 (TREMBLrel. 15, last sequence update)
 DE METALLOTHIONEIN (FRAGMENT).
 GN MT.
 OS Ruditapes philippinarum.
 CC Eukaryota; Metazoa; Mollusca; Bivalvia; Heteroconchia; Veneroidea;
 CC Veneroidea; Veneridae; Ruditapes.
 NCBI_TaxID=104384;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=GILL;
 RA Moraga D., Tanquy A.;
 RT "Characterisation of metallothioneins sequences in three clams
 RT Ruditapes decussatus, Ruditapes philippinarum and Venerupis
 RT pullastra".
 RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AJ249686; CAB96403.1; -;
 FT NON_TER 1
 FT SEQUENCE 57 AA; 5411 MW; F7B37567623FD7DD CRC64;

Query Match 100.0%; Score 54; DB 5; Length 57;
 Best Local Similarity 18.2%; Pred. No. 88;
 Matches 4; Conservative 18; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CXXXCXXXXXXXXXXCXXC 22
 Db 12 CSDSCPATGCKGCGCKGCGDC 33

Q90623
 ID 090623 PRELIMINARY; PRT; 58 AA.
 AC 090623;
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, last sequence update)
 DT 01-OCT-2000 (TREMBLrel. 15, last annotation update)
 DE METALLOTHIONEIN.
 OS Pacifastacus leniusculus (Signal crayfish).
 CC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
 CC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Astacidea;
 CC Astacoidae; Astacidae; Pacifastacus.
 NCBI_TaxID=6720;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=THORACIC GANGLIA;
 RA Skorupski P., Dawbarn D.;
 RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF199482; AAF07215.1; -;
 DR HSSP; P55949; 1DMC.
 DR INTERPRO: IPR002045; -;
 DR INTERPRO: IPR003019; -;
 DR PFAM; PF00131; metalchio.1.
 DR PRINTS; PR00858; MTCRUSTACEAN.
 FT NON_TER 1
 FT SEQUENCE 58 AA; 6008 MW; 576635ACFB0E5100 CRC64;

Query Match 100.0%; Score 54; DB 5; Length 58;
 Best Local Similarity 18.2%; Pred. No. 89;
 Matches 4; Conservative 18; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CXXXCXXXXXXXXXXCXXC 22
 Db 17 CKTGCVCTSCRCPCDCKCTSGC 38

RESULT 13
 ID 09N9H1 PRELIMINARY; PRT; 59 AA.
 AC 09N9H1;
 DT 01-OCT-2000 (TREMBLrel. 15, Created)
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
 DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
 DE METALLOTHIONEIN (FRAGMENT).
 GN MT.
 OS Ruditapes decussatus.
 OC Eukaryota; Metazoa; Mollusca; Bivalvia; Heteroconchia; Veneroidea;
 OC Veneroidea; Veneridae; Ruditapes.
 OX NCBI_TaxID=104385;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=GILL;
 RA Moraga D., Tanguy A.;
 RT "Characterisation of metallothionein sequences in three classes of
 RT Ruditapes decussatus, Ruditapes philippinarum and Venerup
 RT pullastra".
 RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL: A249687; CAB96402.1;
 FT NON_TER 1 50
 FT NON_TER 59 50
 FT SEQUENCE 59 AA; 5613 MM; CAB87C9FE35EC8A2 CRC64;

Query Match 100.0%; Score 54; DB 5; Length 59;
 Best Local Similarity 18.2%; Pred. No. 90;
 Matches 4; Conservative 18; Mismatches 0; Indels 0; Gaps 0;

QY 1 CXXXXXXXXXXXXXXXXX 22
 ID 14 CDSOCPATCKCKGCGCKGCGC 35

RESULT 14
 ID 065918 PRELIMINARY; PRT; 62 AA.
 AC 065918;
 DT 01-AUG-1998 (TREMBLrel. 07, Created)
 DT 01-AUG-1998 (TREMBLrel. 07, Last sequence update)
 DT 01-NOV-1999 (TREMBLrel. 12, Last annotation update)
 DE GAS5-LIKE PROTEIN (FRAGMENT).
 GN SB35.
 OS Picea mariana (Black spruce).
 OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
 OC Coniferopsida; Coniferales; Pinaceae; Picea.
 OX NCBI_TaxID=3335;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Peary D.J., Bousquet J.;
 RL Genetics 0:0-0(1998).
 DR EMBL: AF051754; AAC32171.1;
 DR EMBL: AF051753; AAC32170.1;
 DR EMBL: 29301; Picma; 1249; 29301.
 FT NON_TER 1 1
 FT SEQUENCE 62 AA; 6886 MM; A576222C14631F35 CRC64;

Query Match 100.0%; Score 54; DB 10; Length 62;
 Best Local Similarity 18.2%; Pred. No. 93;
 Matches 4; Conservative 18; Mismatches 0; Indels 0; Gaps 0;

QY 1 CXXXXXXXXXXXXXXXXX 22
 ID 4 CGGRCYSRCSATSHKKPCMFEC 25

RESULT 15
 ID 09VE14 PRELIMINARY; PRT; 66 AA.

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AC 09VE14;
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-MAY-2000 (TREMBLrel. 13, Last annotation update)
 DE CG7606 PROTEIN.
 GN CG7606.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephyridae; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BERKELEY;
 RA MEDLINE=20196006; Pubmed=10731132;
 RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.-H.C., Blaise R.G., Champe M., Pfeiffer B.D.,
 RA Man K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
 RA Adair J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
 RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Bernan B.P., Biadatti D., Bolshakov S.,
 RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,
 RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Dou P.L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferrelia S., Fleischmann W.,
 RA Foster C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
 RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
 RA Hosten D., Houston K.A., Howland T.J., Wei M.-H., Iqbal C.,
 RA Jabali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kuip D., Lai Z.,
 RA Laake P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Paclik J.M.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Svirkas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weissbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of Drosophila melanogaster."
 RL Science 287:2185-2195(2000).
 DR EMBL: AE003718; AAF5437.1;
 DR FLYBASE: FBgn0040565; CG7606.
 SQ SEQUENCE 66 AA; 6812 MM; 8151A9DB3BF85FC CRC64;

Query Match 100.0%; Score 54; DB 5; Length 66;
 Best Local Similarity 18.2%; Pred. No. 96;
 Matches 4; Conservative 18; Mismatches 0; Indels 0; Gaps 0;

QY 1 CXXXXXXXXXXXXXXXXX 22
 ID 30 CGGCGCKPQCLSCGSRSCGCGC 51

Search completed: March 1, 2001, 16:22:09
 Job time: 286 sec

